OIPE IAP20 JAN 27 2006 PATENT & TRADEMARK OFFICE

SEQUENCE LISTING

<110> Suntory Limited

<110> Nippon Paper Industries

<120> Gene coding for protein participating in signal transduction of cytokinin

<130> 993776

<160> 2

<210> 1

<211> 3096

<212> DNA

<213> Arabidopsis thaliana

<221> CDS

<222> (187)...(2952)

<223> Nucleotide sequence coding for histidine protein kinase

<400> 1

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gtttgaattt tgagatttgt ctggtccatt gtgttgctgt tgttgtatga agagaaacct  180
tgatca atg gtc tgt gaa atg gag act gat cag att gag gaa atg gat      228
       Met Val Cys Glu Met Glu Thr Asp Gln Ile Glu Glu Met Asp
         1               5                  10
gtc gaa gtt ttg tct tcg atg tgg ccc gaa gat gtt gga act gaa gct    276
Val Glu Val Leu Ser Ser Met Trp Pro Glu Asp Val Gly Thr Glu Ala
 15                  20                  25                  30
gac aaa cag ttc aac gtc gag aaa cct gcc gga gat tta gac acg ttg    324
Asp Lys Gln Phe Asn Val Glu Lys Pro Ala Gly Asp Leu Asp Thr Leu
                 35                  40                  45
aaa gaa gtt act atc gag aca cgg acc att gcg gat atg aca cgg tta    372
Lys Glu Val Thr Ile Glu Thr Arg Thr Ile Ala Asp Met Thr Arg Leu
             50                  55                  60
cca aac cta ttg aat tcg act cat caa ggc tcc tct caa cta acc aac    420
Pro Asn Leu Leu Asn Ser Thr His Gln Gly Ser Ser Gln Leu Thr Asn
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aaa gaa gag cta aaa aat ctc gat aga cag aga gaa gaa gcc gag gct    516
Lys Glu Glu Leu Lys Asn Leu Asp Arg Gln Arg Glu Glu Ala Glu Ala
 95                 100                 105                 110
aaa gag ttg aag atc att gag gag tat aag ttt gag agc aac gag cct    564
Lys Glu Leu Lys Ile Ile Glu Glu Tyr Lys Phe Glu Ser Asn Glu Pro
                115                 120                 125
gag aat gtt ccg gtt ttg gat gag acg agt gat ttg ttc cgc agg ttt    612
Glu Asn Val Pro Val Leu Asp Glu Thr Ser Asp Leu Phe Arg Arg Phe
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agg cag aaa aaa cga gat gcc ttg gtc gat agc aag aag att gag atc    660
Arg Gln Lys Lys Arg Asp Ala Leu Val Asp Ser Lys Lys Ile Glu Ile
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tat gag gag ttt gac act gtt gca tat tgg aaa cag aag gcg ttg agt    708
Tyr Glu Glu Phe Asp Thr Val Ala Tyr Trp Lys Gln Lys Ala Leu Ser
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ctt gag aaa atg ctt gag gcg agt act gag aga gaa agg cga ttg atg    756
Leu Glu Lys Met Leu Glu Ala Ser Thr Glu Arg Glu Arg Arg Leu Met
170                 180                 185                 190
gag aag ctg agt gag agt ttg aaa act atg gag agt cag tca gca ccg    804
Glu Lys Leu Ser Glu Ser Leu Lys Thr Met Glu Ser Gln Ser Ala Pro
                195                 200                 205
gtc caa gag ctt act cag aat ctt aag aga gct gaa ggt ttc ttg cat    852
Val Gln Glu Leu Thr Gln Asn Leu Lys Arg Ala Glu Gly Phe Leu His
            210                 215                 220
ttc ata ctt cag aat gca cct att gtt atg ggc cat cag gat aaa gat    900
Phe Ile Leu Gln Asn Ala Pro Ile Val Met Gly His Gln Asp Lys Asp
        225                 230                 235
tta cgc tac ttg ttc atc tac aac aag tat cct agt tta cgg gaa cag    948
Leu Arg Tyr Leu Phe Ile Tyr Asn Lys Tyr Pro Ser Leu Arg Glu Gln
    240                 245                 250
gac att ttg gga aaa aca gac gtg gag ata ttc cat gga ggt gga gtt    996
Asp Ile Leu Gly Lys Thr Asp Val Glu Ile Phe His Gly Gly Gly Val
255                 260                 265                 270
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aaa gaa tct gaa gat ttc aag aga gaa gtt ctt gag aaa gga aaa gct   1044
Lys Glu Ser Glu Asp Phe Lys Arg Glu Val Leu Glu Lys Gly Lys Ala
                275                 280                 285
tca aag aga gag atc aca ttt act aca gat tta ttt gga tca aag acg   1092
Ser Lys Arg Glu Ile Thr Phe Thr Thr Asp Leu Phe Gly Ser Lys Thr
            290                 295                 300
ttt ttg ata tat gtt gag cct gtt tac aac aaa gct ggc gag aaa atc   1140
Phe Leu Ile Tyr Val Glu Pro Val Tyr Asn Lys Ala Gly Glu Lys Ile
        305                 310                 315
ggt ata aac tac atg gga atg gaa gta act gat cag gta gtg aaa agg   1188
Gly Ile Asn Tyr Met Gly Met Glu Val Thr Asp Gln Val Val Lys Arg
    320                 325                 330
gag aaa atg gcg aaa ctt aga gaa gat aac gct gtg aga aag gcg atg   1236
Glu Lys Met Ala Lys Leu Arg Glu Asp Asn Ala Val Arg Lys Ala Met
335                 340                 345                 350
gaa tca gaa ctg aac aag act att cac att aca gag gag aca atg aga   1284
Glu Ser Glu Leu Asn Lys Thr Ile His Ile Thr Glu Glu Thr Met Arg
                355                 360                 365
gca aag cag atg cta gcg acg atg tct cat gag ata agg tca cca ttg   1332
Ala Lys Gln Met Leu Ala Thr Met Ser His Glu Ile Arg Ser Pro Leu
            370                 375                 380
tca gga gta gtg gga atg gct gag ata ctt tca act aca aaa ctg gat   1380
Ser Gly Val Val Gly Met Ala Glu Ile Leu Ser Thr Thr Lys Leu Asp
        385                 390                 395
aaa gag caa aga cag ttg ttg aat gtc atg atc tct tct ggt gat ttg   1428
Lys Glu Gln Arg Gln Leu Leu Asn Val Met Ile Ser Ser Gly Asp Leu
    400                 405                 410
gtg ctt cag cta atc aac gac att ctt gat ctc tcc aag gtt gaa tca   1476
Val Leu Gln Leu Ile Asn Asp Ile Leu Asp Leu Ser Lys Val Glu Ser
415                 420                 425                 430
ggt gtg atg aga tta gaa gct aca aag ttt cga cca aga gaa gta gtg   1524
Gly Val Met Arg Leu Glu Ala Thr Lys Phe Arg Pro Arg Glu Val Val
                435                 440                 445
aag cat gtg cta cag aca gct gca gca tcg ctg aag aaa tct ttg aca   1572
Lys His Val Leu Gln Thr Ala Ala Ala Ser Leu Lys Lys Ser Leu Thr
            450                 455                 460
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tta gaa gga aac att gca gat gat gtt cct att gag gta gtt gga gat   1620
Leu Glu Gly Asn Ile Ala Asp Asp Val Pro Ile Glu Val Val Gly Asp
        465                 470                 475
gtt cta agg att agg cag atc ctc acc aat ttg ata agc aat gct atc   1668
Val Leu Arg Ile Arg Gln Ile Leu Thr Asn Leu Ile Ser Asn Ala Ile
    480                 485                 490
aag ttt aca cat gaa gga aat gta gga atc aaa ctc caa gtg ata tca   1716
Lys Phe Thr His Glu Gly Asn Val Gly Ile Lys Leu Gln Val Ile Ser
495                 500                 505                 510
gaa cca tcc ttt gtg cgg gat aac gca ttg aac gca gac acc gag gaa   1764
Glu Pro Ser Phe Val Arg Asp Asn Ala Leu Asn Ala Asp Thr Glu Glu
                515                 520                 525
cac gaa caa aac ggt ttg acc gag act tca gtt tgg att tgc tgt gac   1812
His Glu Gln Asn Gly Leu Thr Glu Thr Ser Val Trp Ile Cys Cys Asp
            530                 535                 540
gta tgg gac act gga att gga atc cca gaa aac gct ctt cca tgt ttg   1860
Val Trp Asp Thr Gly Ile Gly Ile Pro Glu Asn Ala Leu Pro Cys Leu
        545                 550                 555
ttc aag aag tac atg caa gca agc gct gat cat gcc cgg aaa tac ggt   1908
Phe Lys Lys Tyr Met Gln Ala Ser Ala Asp His Ala Arg Lys Tyr Gly
    560                 565                 570
ggg act ggt ctc gga ctt gct att tgt aaa cag ctg gtt gag tta atg   1956
Gly Thr Gly Leu Gly Leu Ala Ile Cys Lys Gln Leu Val Glu Leu Met
575                 580                 585                 590
gga ggc caa ctc act gtg aca agc cgg gtg agc gaa ggt tca acg ttc   2004
Gly Gly Gln Leu Thr Val Thr Ser Arg Val Ser Glu Gly Ser Thr Phe
                595                 600                 605
aca ttt ata tta ccc tac aaa gtt gga aga tca gat gat tat tca gat   2052
Thr Phe Ile Leu Pro Tyr Lys Val Gly Arg Ser Asp Asp Tyr Ser Asp
            610                 615                 620
gat caa gat gag ttc tct gat atg gcg gat caa caa tct gaa cca gac   2100
Asp Gln Asp Glu Phe Ser Asp Met Ala Asp Gln Gln Ser Glu Pro Asp
        625                 630                 635
gat aca gct gaa gga tat ttc cag ttt aaa ccg ctc tta gga tcg ata   2148
Asp Thr Ala Glu Gly Tyr Phe Gln Phe Lys Pro Leu Leu Gly Ser Ile
    640                 645                 650
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tat tcg aat ggc gga ccg ggg atc agc aat gac ttc tta cct cat aaa   2196
Tyr Ser Asn Gly Gly Pro Gly Ile Ser Asn Asp Phe Leu Pro His Lys
655                 660                 665                 670
gtc atg ctt act agt cct att aag ctc atc aat ggt ttt gtc gct gat   2244
Val Met Leu Thr Ser Pro Ile Lys Leu Ile Asn Gly Phe Val Ala Asp
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ccc tct aat aac act gga cag agc gag atg cta cag ctt gaa aac ggt   2292
Pro Ser Asn Asn Thr Gly Gln Ser Glu Met Leu Gln Leu Glu Asn Gly
            690                 695                 700
ggt tac atg gat gaa tct aaa ctc gaa acc agt tct ggt cat tgc cct   2340
Gly Tyr Met Asp Glu Ser Lys Leu Glu Thr Ser Ser Gly His Cys Pro
        705                 710                 715
gaa tca gct cac caa tat gag aat gga aat ggt cga tgt ttc tct aag   2388
Glu Ser Ala His Gln Tyr Glu Asn Gly Asn Gly Arg Cys Phe Ser Lys
    720                 725                 730
gaa tct gaa tct tgt agc agt tca caa gct agc tca gaa ggt gga acc   2436
Glu Ser Glu Ser Cys Ser Ser Ser Gln Ala Ser Ser Glu Gly Gly Thr
735                 740                 745                 750
tta gaa atg gag tca gag ctc aca gtt tca tct cat agg gaa gag gaa   2484
Leu Glu Met Glu Ser Glu Leu Thr Val Ser Ser His Arg Glu Glu Glu
                755                 760                 765
aaa gcc gag aca gaa gta aaa gaa aca tca aag cca aag att ttg ctt   2532
Lys Ala Glu Thr Glu Val Lys Glu Thr Ser Lys Pro Lys Ile Leu Leu
            770                 775                 780
gtg gaa gat aat aag atc aac atc atg gtt gca aag tcg atg atg aag   2580
Val Glu Asp Asn Lys Ile Asn Ile Met Val Ala Lys Ser Met Met Lys
        785                 790                 795
cag tta ggc cat acc atg gat att gct aat aat gga gtt gaa gcc ata   2628
Gln Leu Gly His Thr Met Asp Ile Ala Asn Asn Gly Val Glu Ala Ile
    800                 805                 810
acc gcg att aat agc tct agc tac gat ctg gta ctc atg gat gtg tgc   2676
Thr Ala Ile Asn Ser Ser Ser Tyr Asp Leu Val Leu Met Asp Val Cys
815                 820                 825                 830
atg ccg gtg ctc gat ggt tta aaa gct aca aga ctg atc cgt tcg tat   2724
Met Pro Val Leu Asp Gly Leu Lys Ala Thr Arg Leu Ile Arg Ser Tyr
                835                 840                 845
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gaa gaa act ggg aac tgg aat gct gca ata gaa gcc gga gta gat ata   2772
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            850                 855                 860
tcg aca tcg gag aat gaa caa gtt tgt atg cgt ccc aca aac cgg ctg   2820
Ser Thr Ser Glu Asn Glu Gln Val Cys Met Arg Pro Thr Asn Arg Leu
        865                 870                 875
cct ata atc gcg atg acg gca aat act tta gca gag agt tca gaa gaa   2868
Pro Ile Ile Ala Met Thr Ala Asn Thr Leu Ala Glu Ser Ser Glu Glu
    880                 885                 890
tgt tat gca aat ggt atg gac tcg ttt att tcg aaa cct gta acg ttg   2916
Cys Tyr Ala Asn Gly Met Asp Ser Phe Ile Ser Lys Pro Val Thr Leu
895                 900                 905                 910
caa aaa ctg aga gag tgt ttg caa cag tat ttg cac tgagatttca        2962
Gln Lys Leu Arg Glu Cys Leu Gln Gln Tyr Leu His
                915                 920
gatttttgtg ttttgtagat taagaaatgg ttgtgttgta tataaattgt gtaggaaaaa 3022
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<213> Arabidopsis thaliana

<223> Amino acid sequence of histidine protein kinase

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Val Thr Ile Glu Thr Arg Thr Ile Ala Asp Met Thr Arg Leu Pro Asn
     50                  55                  60
Leu Leu Asn Ser Thr His Gln Gly Ser Ser Gln Leu Thr Asn Leu Val
 65                  70                  75                  80
Lys Gln Trp Glu Tyr Met Gln Asp Asn Ala Val Arg Leu Leu Lys Glu
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            100                 105                 110
Leu Lys Ile Ile Glu Glu Tyr Lys Phe Glu Ser Asn Glu Pro Glu Asn
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Val Pro Val Leu Asp Glu Thr Ser Asp Leu Phe Arg Arg Phe Arg Gln
    130                 135                 140
Lys Lys Arg Asp Ala Leu Val Asp Ser Lys Lys Ile Glu Ile Tyr Glu
145                 150                 155                 160
Glu Phe Asp Thr Val Ala Tyr Trp Lys Gln Lys Ala Leu Ser Leu Glu
                165                 170                 175
Lys Met Leu Glu Ala Ser Thr Glu Arg Glu Arg Arg Leu Met Glu Lys
            180                 185                 190
Leu Ser Glu Ser Leu Lys Thr Met Glu Ser Gln Ser Ala Pro Val Gln
        195                 200                 205
Glu Leu Thr Gln Asn Leu Lys Arg Ala Glu Gly Phe Leu His Phe Ile
    210                 215                 220
Leu Gln Asn Ala Pro Ile Val Met Gly His Gln Asp Lys Asp Leu Arg
225                 230                 235                 240
Tyr Leu Phe Ile Tyr Asn Lys Tyr Pro Ser Leu Arg Glu Gln Asp Ile
                245                 250                 255
Leu Gly Lys Thr Asp Val Glu Ile Phe His Gly Gly Gly Val Lys Glu
            260                 265                 270
Ser Glu Asp Phe Lys Arg Glu Val Leu Glu Lys Gly Lys Ala Ser Lys
        275                 280                 285
Arg Glu Ile Thr Phe Thr Thr Asp Leu Phe Gly Ser Lys Thr Phe Leu
    290                 295                 300
Ile Tyr Val Glu Pro Val Tyr Asn Lys Ala Gly Glu Lys Ile Gly Ile
305                 310                 315                 320
Asn Tyr Met Gly Met Glu Val Thr Asp Gln Val Val Lys Arg Glu Lys
                325                 330                 335
Met Ala Lys Leu Arg Glu Asp Asn Ala Val Arg Lys Ala Met Glu Ser
            340                 345                 350
Glu Leu Asn Lys Thr Ile His Ile Thr Glu Glu Thr Met Arg Ala Lys
        355                 360                 365
Gln Met Leu Ala Thr Met Ser His Glu Ile Arg Ser Pro Leu Ser Gly
    370                 375                 380
Val Val Gly Met Ala Glu Ile Leu Ser Thr Thr Lys Leu Asp Lys Glu
385                 390                 395                 400
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405 410 415
Gln Leu Ile Asn Asp Ile Leu Asp Leu Ser Lys Val Glu Ser Gly Val
420 425 430
Met Arg Leu Glu Ala Thr Lys Phe Arg Pro Arg Glu Val Val Lys His
435 440 445
Val Leu Gln Thr Ala Ala Ala Ser Leu Lys Lys Ser Leu Thr Leu Glu
450 455 460
Gly Asn Ile Ala Asp Asp Val Pro Ile Glu Val Val Gly Asp Val Leu
465 470 475 480
Arg Ile Arg Gln Ile Leu Thr Asn Leu Ile Ser Asn Ala Ile Lys Phe
485 490 495
Thr His Glu Gly Asn Val Gly Ile Lys Leu Gln Val Ile Ser Glu Pro
500 505 510
Ser Phe Val Arg Asp Asn Ala Leu Asn Ala Asp Thr Glu Glu His Glu
515 520 525
Gln Asn Gly Leu Thr Glu Thr Ser Val Trp Ile Cys Cys Asp Val Trp
530 535 540
Asp Thr Gly Ile Gly Ile Pro Glu Asn Ala Leu Pro Cys Leu Phe Lys
545 550 555 560
Lys Tyr Met Gln Ala Ser Ala Asp His Ala Arg Lys Tyr Gly Gly Thr
565 570 575
Gly Leu Gly Leu Ala Ile Cys Lys Gln Leu Val Glu Leu Met Gly Gly
580 585 590
Gln Leu Thr Val Thr Ser Arg Val Ser Glu Gly Ser Thr Phe Thr Phe
595 600 605
Ile Leu Pro Tyr Lys Val Gly Arg Ser Asp Asp Tyr Ser Asp Asp Gln
610 615 620
Asp Glu Phe Ser Asp Met Ala Asp Gln Gln Ser Glu Pro Asp Asp Thr
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Ala Glu Gly Tyr Phe Gln Phe Lys Pro Leu Leu Gly Ser Ile Tyr Ser
645 650 655
Asn Gly Gly Pro Gly Ile Ser Asn Asp Phe Leu Pro His Lys Val Met
660 665 670
Leu Thr Ser Pro Ile Lys Leu Ile Asn Gly Phe Val Ala Asp Pro Ser
675 680 685
Asn Asn Thr Gly Gln Ser Glu Met Leu Gln Leu Glu Asn Gly Gly Tyr
690 695 700

Met Asp Glu Ser Lys Leu Glu Thr Ser Ser Gly His Cys Pro Glu Ser
705 710 715 720
Ala His Gln Tyr Glu Asn Gly Asn Gly Arg Cys Phe Ser Lys Glu Ser
725 730 735
Glu Ser Cys Ser Ser Ser Gln Ala Ser Ser Glu Gly Gly Thr Leu Glu
740 745 750
Met Glu Ser Glu Leu Thr Val Ser Ser His Arg Glu Glu Glu Lys Ala
755 760 765
Glu Thr Glu Val Lys Glu Thr Ser Lys Pro Lys Ile Leu Leu Val Glu
770 775 780
Asp Asn Lys Ile Asn Ile Met Val Ala Lys Ser Met Met Lys Gln Leu
785 790 795 800
Gly His Thr Met Asp Ile Ala Asn Asn Gly Val Glu Ala Ile Thr Ala
805 810 815
Ile Asn Ser Ser Ser Tyr Asp Leu Val Leu Met Asp Val Cys Met Pro
820 825 830
Val Leu Asp Gly Leu Lys Ala Thr Arg Leu Ile Arg Ser Tyr Glu Glu
835 840 845
Thr Gly Asn Trp Asn Ala Ala Ile Glu Ala Gly Val Asp Ile Ser Thr
850 855 860
Ser Glu Asn Glu Gln Val Cys Met Arg Pro Thr Asn Arg Leu Pro Ile
865 870 875 880
Ile Ala Met Thr Ala Asn Thr Leu Ala Glu Ser Ser Glu Glu Cys Tyr
885 890 895
Ala Asn Gly Met Asp Ser Phe Ile Ser Lys Pro Val Thr Leu Gln Lys
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<223> Nucleotide sequence of genomic DNA coding for histidine protein kinase

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aaattaccaa tctttcacaa ttcattcaca tgctcctctc tctttcttca ttggctattc 180

tcttcccaat gctcatttga agtttattta ctctactccc gacgaccacg actcttcttc 240

agatctactc actccttctt tctctccttc ttcttcttca tttttccggt gaccggagtc 300

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ggagaaggta aagcttctga tcccttcccc tttcctccgg catactcgtt cctctgcttt   360
gtctttcgtt tttttcattt ctttctgttt cagccttttg catctcgaga cttcatgatt   420
acaatttctt tatgtttctc aatgcaagat tttcgtttat aatatatgat cactgatgtc   480
aagaataaat caccaaagat ttttttcttt ccatatattt tttccgatca tcgctcaaaa   540
aaaagtttca tcgtttaaat ttattttcag attttatcgt ttattggtga attttatgat   600
cctagttgat aattcaatct gaaaaaagaa actgatacag ttttcttttt gaagctctgc   660
aaatttctga tttttaagct cgaatcatat aatttgaagt ttcccgctaa tgttcaatca   720
gaattggtcc acacacttag ttgttgtgga ccctttgcaa aattctattt tagttcatta   780
tttttcacat tttacagatc aagattctct gatggagatg gtttgtcctg actctaacct   840
ctgtgtttga aaatatctat acaggttctt tattcagatc aaggttctgg cttaaagaaa   900
aaagttgttt gaattttgag atttgtctgg tccattgtgt tgctgttgtt gtatgaagag   960
aaaccttgat ca                                                      972
atg gtc tgt gaa atg gag act gat cag att gag gaa atg gat gtc gaa    1020
Met Val Cys Glu Met Glu Thr Asp Gln Ile Glu Glu Met Asp Val Glu
  1               5                  10                  15
gtt ttg tct tcg atg tgg ccc gaa gat gtt gga act gaa gct gac aaa    1068
Val Leu Ser Ser Met Trp Pro Glu Asp Val Gly Thr Glu Ala Asp Lys
             20                  25                  30
cag ttc aac gtc gag aaa cct gcc gga gat tta gac acg ttg aaa gaa    1116
Gln Phe Asn Val Glu Lys Pro Ala Gly Asp Leu Asp Thr Leu Lys Glu
         35                  40                  45
gtt act atc gag aca cgg acc att gcg gat atg aca cgg tta cca aac    1164
Val Thr Ile Glu Thr Arg Thr Ile Ala Asp Met Thr Arg Leu Pro Asn
     50                  55                  60
cta ttg aat tcg act cat caa ggc tcc tct caa cta acc aac ctt gtg    1212
Leu Leu Asn Ser Thr His Gln Gly Ser Ser Gln Leu Thr Asn Leu Val
 65                  70                  75                  80
aaa caa tgg gag tat atg caa gac aac gcg gtt cgg ctg tta aaa gaa    1260
Lys Gln Trp Glu Tyr Met Gln Asp Asn Ala Val Arg Leu Leu Lys Glu
                 85                  90                  95
gag cta aaa aat ctc gat aga cag aga gaa gaa gcc gag gct aaa gag    1308
Glu Leu Lys Asn Leu Asp Arg Gln Arg Glu Glu Ala Glu Ala Lys Glu
            100                 105                 110
ttg aag atc att gag gag tat aag ttt gag agc aac gag cct gag aat    1356
Leu Lys Ile Ile Glu Glu Tyr Lys Phe Glu Ser Asn Glu Pro Glu Asn
        115                 120                 125
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gtt ccg gtt ttg gat gag acg agt gat ttg ttc cgc agg ttt agg cag   1404
Val Pro Val Leu Asp Glu Thr Ser Asp Leu Phe Arg Arg Phe Arg Gln
    130                 135                 140
aaa aaa cga gat gcc ttg gtc gat agc aag aag att gag atc tat gag   1452
Lys Lys Arg Asp Ala Leu Val Asp Ser Lys Lys Ile Glu Ile Tyr Glu
145                 150                 155                 160
gag ttt gac act gtt gca tat tgg aaa cag aag gcg ttg agt ctt gag   1500
Glu Phe Asp Thr Val Ala Tyr Trp Lys Gln Lys Ala Leu Ser Leu Glu
                165                 170                 175
aaa atg ctt gag gcg agt act gag aga gaa agg cga ttg atg gag aag   1548
Lys Met Leu Glu Ala Ser Thr Glu Arg Glu Arg Arg Leu Met Glu Lys
            180                 185                 190
ctg agt gag agt ttg aaa act atg gag agt cag tca gca ccg gtc caa   1596
Leu Ser Glu Ser Leu Lys Thr Met Glu Ser Gln Ser Ala Pro Val Gln
        195                 200                 205
gag ctt act cag aat ctt aag aga gct gaa ggt ttc ttg cat ttc ata   1644
Glu Leu Thr Gln Asn Leu Lys Arg Ala Glu Gly Phe Leu His Phe Ile
    210                 215                 220
ctt cag aat gca cct att gtt atg ggc cat cag gtaaagtaaa aggtgattct 1697
Leu Gln Asn Ala Pro Ile Val Met Gly His Gln
225                 230                 235
tgatcttgtt ttcgatcttt tcgacttttc tgattctttg ttacttatga gtttcag    1754
gat aaa gat tta cgc tac ttg ttc atc tac aac aag tat cct agt tta   1802
Asp Lys Asp Leu Arg Tyr Leu Phe Ile Tyr Asn Lys Tyr Pro Ser Leu
                240                 245                 250
cgg gaa cag gttagaagaa aacttttttct tctgttggat ttattgaatc          1851
Arg Glu Gln
attctctgag gaaatgtgtt taaatcaaaa tctgtttctt actatatttc ag gac     1906
                                                          Asp
                                                          255
att ttg gga aaa aca gac gtg gag ata ttc cat gga ggt gga gtt aaa   1954
Ile Leu Gly Lys Thr Asp Val Glu Ile Phe His Gly Gly Gly Val Lys
                260                 265                 270
gaa tct gaa gat ttc aag aga gaa gtt ctt gag aaa gga aaa gct tca   2002
Glu Ser Glu Asp Phe Lys Arg Glu Val Leu Glu Lys Gly Lys Ala Ser
            275                 280                 285
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aag aga gag atc aca ttt act aca gat tta ttt gga tca aag acg ttt   2050
Lys Arg Glu Ile Thr Phe Thr Thr Asp Leu Phe Gly Ser Lys Thr Phe
        290                 295                 300
ttg ata tat gtt gag cct gtt tac aac aaa gct ggc gag aaa atc ggt   2098
Leu Ile Tyr Val Glu Pro Val Tyr Asn Lys Ala Gly Glu Lys Ile Gly
    305                 310                 315
ata aac tac atg gga atg gaa gta act gat cag gttagttagc taaagatttt 2151
Ile Asn Tyr Met Gly Met Glu Val Thr Asp Gln
320                 325                 330
tgaactattc tataatctat gttctcattt tcacatcttc actggatctt cctgtgttac 2211
ag gta gtg aaa agg gag aaa atg gcg aaa ctt aga gaa gat aac gct    2258
   Val Val Lys Arg Glu Lys Met Ala Lys Leu Arg Glu Asp Asn Ala
                  335                 340                 345
gtg aga aag gcg atg gaa tca gaa ctg aac aag act att cac att aca   2306
Val Arg Lys Ala Met Glu Ser Glu Leu Asn Lys Thr Ile His Ile Thr
               350                 355                 360
g gtttgttcaa gttaagcagt gaaagtttta gaaagattaa tgagaaaact          2357
agacttaggt gttgtgtttt ttcttttgca g ag gag aca atg aga gca aag cag 2411
                                  Glu Glu Thr Met Arg Ala Lys Gln
                                                  365
atg cta gcg acg atg tct cat gag ata agg tca cca ttg tca gga gta   2459
Met Leu Ala Thr Met Ser His Glu Ile Arg Ser Pro Leu Ser Gly Val
370                 375                 380                 385
gtg gga atg gct gag ata ctt tca act aca aaa ctg gat aaa gag caa   2507
Val Gly Met Ala Glu Ile Leu Ser Thr Thr Lys Leu Asp Lys Glu Gln
               390                 395                 400
aga cag ttg ttg aat gtc atg atc tct tct ggt gat ttg gtg ctt cag   2555
Arg Gln Leu Leu Asn Val Met Ile Ser Ser Gly Asp Leu Val Leu Gln
            405                 410                 415
cta atc aac gac att ctt gat ctc tcc aag gtt gaa tca g gtacaatata  2605
Leu Ile Asn Asp Ile Leu Asp Leu Ser Lys Val Glu Ser
        420                 425                 430
ctgttttcaa agtttttgat cttgtggtgt ggtcattgtt caaatcctcg attacatatg 2665
ttatttttg gtatttgtgt gttcttttta g gt gtg atg aga tta gaa gct aca 2719
                                  Gly Val Met Arg Leu Glu Ala Thr
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aag ttt cga cca aga gaa gta gtg aag cat gtg cta cag aca gct gca   2767
Lys Phe Arg Pro Arg Glu Val Val Lys His Val Leu Gln Thr Ala Ala
    440                 445                 450
gca tcg ctg aag aaa tct ttg aca tta gaa gga aac att gca gat gat   2815
Ala Ser Leu Lys Lys Ser Leu Thr Leu Glu Gly Asn Ile Ala Asp Asp
455                 460                 465                 470
gtt cct att gag gttactacac atttcagaaa gagttaaatg tggcaaaagt       2867
Val Pro Ile Glu
ctttgtgatc ttaacttttt ttcctttaaa tgtttag gta gtt gga gat gtt cta  2922
                                        Val Val Gly Asp Val Leu
                                        475                 480
agg att agg cag atc ctc acc aat ttg ata ag gttctttacc tgattcctgt  2974
Arg Ile Arg Gln Ile Leu Thr Asn Leu Ile Ser
                485                 490
attatttgca taatgacaag tttcggttcc tgatttgttc aaacgttttg cag c aat  3031
                                                            Asn
gct atc aag ttt aca cat gaa gga aat gta gga atc aaa ctc caa gtg   3079
Ala Ile Lys Phe Thr His Glu Gly Asn Val Gly Ile Lys Leu Gln Val
        495                 500                 505
ata tca gaa cca tcc ttt gtg cgg gat aac gca ttg aac gca gac acc   3127
Ile Ser Glu Pro Ser Phe Val Arg Asp Asn Ala Leu Asn Ala Asp Thr
    510                 515                 520
gag gaa cac gaa caa aac ggt ttg acc gag act tca gtt tgg att tgc   3175
Glu Glu His Glu Gln Asn Gly Leu Thr Glu Thr Ser Val Trp Ile Cys
525                 530                 535                 540
tgt gac gta tgg gac act gga att gga atc cca g gcaagcaagc          3219
Cys Asp Val Trp Asp Thr Gly Ile Gly Ile Pro
                545                 550
aattctgaca aatgaacatg aaaagactaa aaaactccaa ctaacctata tattaacctg 3279
gttcatgttt tggtgttctt gtgcag aa aac gct ctt cca tgt ttg ttc aag   3331
                          Glu Asn Ala Leu Pro Cys Leu Phe Lys
                                        555                 560
aag tac atg caa gca agc gct gat cat gcc cgg aaa tac ggt ggg act   3379
Lys Tyr Met Gln Ala Ser Ala Asp His Ala Arg Lys Tyr Gly Gly Thr
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ggt ctc gga ctt gct att tgt aaa cag ctg gtaagctatt attaggattt ta  3431
Gly Leu Gly Leu Ala Ile Cys Lys Gln Leu
            580                 585
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caacacta cagaagaaac taatgaagct cgttatccta atctttcttt gtttgtttac   3489
ag gtt gag tta atg gga ggc caa ctc act gtg aca agc cgg gtg agc     3536
   Val Glu Leu Met Gly Gly Gln Leu Thr Val Thr Ser Arg Val Ser
                590                 595                 600
gaa ggt tca acg ttc aca ttt ata tta ccc tac aaa gtt gga aga tca   3586
Glu Gly Ser Thr Phe Thr Phe Ile Leu Pro Tyr Lys Val Gly Arg Ser
            605                 610                 615
gat gat tat tca gat gat caa gat gag ttc tct gat atg gcg gat caa   3632
Asp Asp Tyr Ser Asp Asp Gln Asp Glu Phe Ser Asp Met Ala Asp Gln
        620                 625                 630
caa tct gaa cca gac gat aca gct gaa gga tat ttc cag ttt aaa ccg   3680
Gln Ser Glu Pro Asp Asp Thr Ala Glu Gly Tyr Phe Gln Phe Lys Pro
    635                 640                 645
ctc tta gga tcg ata tat tcg aat ggc gga ccg ggg atc agc aat gac   3728
Leu Leu Gly Ser Ile Tyr Ser Asn Gly Gly Pro Gly Ile Ser Asn Asp
650                 655                 660                 665
ttc tta cct cat aaa gtc atg ctt act agt cct att aag ctc atc aat   3776
Phe Leu Pro His Lys Val Met Leu Thr Ser Pro Ile Lys Leu Ile Asn
                670                 675                 680
ggt ttt gtc gct gat ccc tct aat aac act gga cag agc gag atg cta   3824
Gly Phe Val Ala Asp Pro Ser Asn Asn Thr Gly Gln Ser Glu Met Leu
            685                 690                 695
cag ctt gaa aac ggt ggt tac atg gat gaa tct aaa ctc gaa acc agt   3872
Gln Leu Glu Asn Gly Gly Tyr Met Asp Glu Ser Lys Leu Glu Thr Ser
        700                 705                 710
tct ggt cat tgc cct gaa tca gct cac caa tat gag aat gga aat ggt   3920
Ser Gly His Cys Pro Glu Ser Ala His Gln Tyr Glu Asn Gly Asn Gly
    715                 720                 725
cga tgt ttc tct aag gaa tct gaa tct tgt agc agt tca caa gct agc   3968
Arg Cys Phe Ser Lys Glu Ser Glu Ser Cys Ser Ser Ser Gln Ala Ser
730                 735                 740                 745
tca gaa ggt gga acc tta gaa atg gag tca gag ctc aca gtt tca tct   4016
Ser Glu Gly Gly Thr Leu Glu Met Glu Ser Glu Leu Thr Val Ser Ser
                750                 755                 760
cat agg gaa gag gaa aaa gcc gag aca gaa gta aaa gaa aca tca aag   4064
His Arg Glu Glu Glu Lys Ala Glu Thr Glu Val Lys Glu Thr Ser Lys
            765                 770                 775
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cca aag att ttg ctt gtg gaa gat aat aag atc aac atc atg gtt gca   4112
Pro Lys Ile Leu Leu Val Glu Asp Asn Lys Ile Asn Ile Met Val Ala
        780                 785                 790
aag tcg atg atg aag cag tta ggc cat acc atg gat att gct aat aat   4160
Lys Ser Met Met Lys Gln Leu Gly His Thr Met Asp Ile Ala Asn Asn
    795                 800                 805
gga gtt gaa gcc ata acc gcg att aat agc tct agc tac gat ctg gta   4208
Gly Val Glu Ala Ile Thr Ala Ile Asn Ser Ser Ser Tyr Asp Leu Val
810                 815                 820                 825
ctc atg gtatgtaaat tttcttagct ctaaggactt gtccttttca aattcactta    4264
Leu Met
tatttgaaaa aggcttataa ttcatattgg gttcacag gat gtg tgc atg ccg gtg 4320
                                        Asp Val Cys Met Pro Val
                                                830
ctc gat ggt tta aaa gct aca aga ctg atc cgt tcg tat gaa gaa act   4368
Leu Asp Gly Leu Lys Ala Thr Arg Leu Ile Arg Ser Tyr Glu Glu Thr
    835                 840                 845
ggg aac tgg aat gct gca ata gaa gcc gga gta gat ata tcg aca tcg   4416
Gly Asn Trp Asn Ala Ala Ile Glu Ala Gly Val Asp Ile Ser Thr Ser
850                 855                 860                 865
gag aat gaa caa gtt tgt atg cgt ccc aca aac cgg ctg cct ata atc   4464
Glu Asn Glu Gln Val Cys Met Arg Pro Thr Asn Arg Leu Pro Ile Ile
                870                 875                 880
gcg gtcagtactt ctttttgaa tactaaacac agagatctaa tgcataactt        4517
Ala
gagaaaactg atagtcagaa tgcgttgtgg aatgtgcag atg acg gca aat act    4571
                                        Met Thr Ala Asn Thr
                                                885
tta gca gag agt tca gaa gaa tgt tat gca aat ggt atg gac tcg ttt   4619
Leu Ala Glu Ser Ser Glu Glu Cys Tyr Ala Asn Gly Met Asp Ser Phe
        890                 895                 900
att tcg aaa cct gta acg ttg caa aaa ctg aga gag tgt ttg caa cag   4667
Ile Ser Lys Pro Val Thr Leu Gln Lys Leu Arg Glu Cys Leu Gln Gln
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Tyr Leu His
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<213> Arabidopsis thariana

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Gln Phe Asn Val Glu Lys Pro Ala Gly Asp Leu Asp Thr Leu Lys Glu
         35                  40                  45
Val Thr Ile Glu Thr Arg Thr Ile Ala Asp Met Thr Arg Leu Pro Asn
     50                  55                  60
Leu Leu Asn Ser Thr His Gln Gly Ser Ser Gln Leu Thr Asn Leu Val
 65                  70                  75                  80
Lys Gln Trp Glu Tyr Met Gln Asp Asn Ala Val Arg Leu Leu Lys Glu
                 85                  90                  95
Glu Leu Lys Asn Leu Asp Arg Gln Arg Glu Glu Ala Glu Ala Lys Glu
            100                 105                 110
Leu Lys Ile Ile Glu Glu Tyr Lys Phe Glu Ser Asn Glu Pro Glu Asn
        115                 120                 125
Val Pro Val Leu Asp Glu Thr Ser Asp Leu Phe Arg Arg Phe Arg Gln
    130                 135                 140
Lys Lys Arg Asp Ala Leu Val Asp Ser Lys Lys Ile Glu Ile Tyr Glu
145                 150                 155                 160
Glu Phe Asp Thr Val Ala Tyr Trp Lys Gln Lys Ala Leu Ser Leu Glu
                165                 170                 175
Lys Met Leu Glu Ala Ser Thr Glu Arg Glu Arg Arg Leu Met Glu Lys
            180                 185                 190
Leu Ser Glu Ser Leu Lys Thr Met Glu Ser Gln Ser Ala Pro Val Gln
        195                 200                 205
Glu Leu Thr Gln Asn Leu Lys Arg Ala Glu Gly Phe Leu His Phe Ile
    210                 215                 220
Leu Gln Asn Ala Pro Ile Val Met Gly His Gln Asp Lys Asp Leu Arg
225                 230                 235                 240
Tyr Leu Phe Ile Tyr Asn Lys Tyr Pro Ser Leu Arg Glu Gln Asp Ile
                245                 250                 255
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Leu Gly Lys Thr Asp Val Glu Ile Phe His Gly Gly Gly Val Lys Glu
260 265 270
Ser Glu Asp Phe Lys Arg Glu Val Leu Glu Lys Gly Lys Ala Ser Lys
275 280 285
Arg Glu Ile Thr Phe Thr Thr Asp Leu Phe Gly Ser Lys Thr Phe Leu
290 295 300
Ile Tyr Val Glu Pro Val Tyr Asn Lys Ala Gly Glu Lys Ile Gly Ile
305 310 315 320
Asn Tyr Met Gly Met Glu Val Thr Asp Gln Val Val Lys Arg Glu Lys
325 330 335
Met Ala Lys Leu Arg Glu Asp Asn Ala Val Arg Lys Ala Met Glu Ser
340 345 350
Glu Leu Asn Lys Thr Ile His Ile Thr Glu Glu Thr Met Arg Ala Lys
355 360 365
Gln Met Leu Ala Thr Met Ser His Glu Ile Arg Ser Pro Leu Ser Gly
370 375 380
Val Val Gly Met Ala Glu Ile Leu Ser Thr Thr Lys Leu Asp Lys Glu
385 390 395 400
Gln Arg Gln Leu Leu Asn Val Met Ile Ser Ser Gly Asp Leu Val Leu
405 410 415
Gln Leu Ile Asn Asp Ile Leu Asp Leu Ser Lys Val Glu Ser Gly Val
420 425 430
Met Arg Leu Glu Ala Thr Lys Phe Arg Pro Arg Glu Val Val Lys His
435 440 445
Val Leu Gln Thr Ala Ala Ala Ser Leu Lys Lys Ser Leu Thr Leu Glu
450 455 460
Gly Asn Ile Ala Asp Asp Val Pro Ile Glu Val Val Gly Asp Val Leu
465 470 475 480
Arg Ile Arg Gln Ile Leu Thr Asn Leu Ile Ser Asn Ala Ile Lys Phe
485 490 495
Thr His Glu Gly Asn Val Gly Ile Lys Leu Gln Val Ile Ser Glu Pro
500 505 510
Ser Phe Val Arg Asp Asn Ala Leu Asn Ala Asp Thr Glu Glu His Glu
515 520 525
Gln Asn Gly Leu Thr Glu Thr Ser Val Trp Ile Cys Cys Asp Val Trp
530 535 540
Asp Thr Gly Ile Gly Ile Pro Glu Asn Ala Leu Pro Cys Leu Phe Lys
545 550 555 560

Lys Tyr Met Gln Ala Ser Ala Asp His Ala Arg Lys Tyr Gly Gly Thr
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Gly Leu Gly Leu Ala Ile Cys Lys Gln Leu Val Glu Leu Met Gly Gly
580 585 590
Gln Leu Thr Val Thr Ser Arg Val Ser Glu Gly Ser Thr Phe Thr Phe
595 600 605
Ile Leu Pro Tyr Lys Val Gly Arg Ser Asp Asp Tyr Ser Asp Asp Gln
610 615 620
Asp Glu Phe Ser Asp Met Ala Asp Gln Gln Ser Glu Pro Asp Asp Thr
625 630 635 640
Ala Glu Gly Tyr Phe Gln Phe Lys Pro Leu Leu Gly Ser Ile Tyr Ser
645 650 655
Asn Gly Gly Pro Gly Ile Ser Asn Asp Phe Leu Pro His Lys Val Met
660 665 670
Leu Thr Ser Pro Ile Lys Leu Ile Asn Gly Phe Val Ala Asp Pro Ser
675 680 685
Asn Asn Thr Gly Gln Ser Glu Met Leu Gln Leu Glu Asn Gly Gly Tyr
690 695 700
Met Asp Glu Ser Lys Leu Glu Thr Ser Ser Gly His Cys Pro Glu Ser
705 710 715 720
Ala His Gln Tyr Glu Asn Gly Asn Gly Arg Cys Phe Ser Lys Glu Ser
725 730 735
Glu Ser Cys Ser Ser Ser Gln Ala Ser Ser Glu Gly Gly Thr Leu Glu
740 745 750
Met Glu Ser Glu Leu Thr Val Ser Ser His Arg Glu Glu Glu Lys Ala
755 760 765
Glu Thr Glu Val Lys Glu Thr Ser Lys Pro Lys Ile Leu Leu Val Glu
770 775 780
Asp Asn Lys Ile Asn Ile Met Val Ala Lys Ser Met Met Lys Gln Leu
785 790 795 800
Gly His Thr Met Asp Ile Ala Asn Asn Gly Val Glu Ala Ile Thr Ala
805 810 815
Ile Asn Ser Ser Ser Tyr Asp Leu Val Leu Met Asp Val Cys Met Pro
820 825 830
Val Leu Asp Gly Leu Lys Ala Thr Arg Leu Ile Arg Ser Tyr Glu Glu
835 840 845
Thr Gly Asn Trp Asn Ala Ala Ile Glu Ala Gly Val Asp Ile Ser Thr
850 855 860

Ser Glu Asn Glu Gln Val Cys Met Arg Pro Thr Asn Arg Leu Pro Ile
865 870 875 880
Ile Ala Met Thr Ala Asn Thr Leu Ala Glu Ser Ser Glu Glu Cys Tyr
885 890 895
Ala Asn Gly Met Asp Ser Phe Ile Ser Lys Pro Val Thr Leu Gln Lys
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915 920

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<221> exon 4

<222> (1243) ··· (1336)

<221> exon 5

<222> (1418) ··· (1624)

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<222> (1726) ··· (1856)

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<222> (1934) ··· (1983)

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<222> (2057) ··· (2238)

<221> exon 9

<222> (2335) ··· (2438)

<221> exon 10

<222> (2521) ··· (3243)

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<223> Nucleotide sequence of genomic DNA coding for histidine protein kinase

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gtt ttg tct tcg atg tgg ccc gaa gat gtt gga act gaa gct gac aaa     96
Val Leu Ser Ser Met Trp Pro Glu Asp Val Gly Thr Glu Ala Asp Lys
             20                  25                  30
cag ttc aac gtc gag aaa cct gcc gga gat tta gac acg ttg aaa gaa    144
Gln Phe Asn Val Glu Lys Pro Ala Gly Asp Leu Asp Thr Leu Lys Glu
         35                  40                  45
gtt act atc gag aca cgg acc att gcg gat atg aca cgg tta cca aac    192
Val Thr Ile Glu Thr Arg Thr Ile Ala Asp Met Thr Arg Leu Pro Asn
     50                  55                  60
cta ttg aat tcg act cat caa ggc tcc tct caa cta acc aac ctt gtg    240
Leu Leu Asn Ser Thr His Gln Gly Ser Ser Gln Leu Thr Asn Leu Val
 65                  70                  75                  80
aaa caa tgg gag tat atg caa gac aac gcg gtt cgg ctg tta aaa gaa    288
Lys Gln Trp Glu Tyr Met Gln Asp Asn Ala Val Arg Leu Leu Lys Glu
                 85                  90                  95
gag cta aag aat ctc gat aga cag aga gaa gaa gct gag gct aaa gag    336
Glu Leu Lys Asn Leu Asp Arg Gln Arg Glu Glu Ala Glu Ala Lys Glu
            100                 105                 110
ttg aag atc att gag gag tat aag ttt gag agc aac gag cct gag aat    384
Leu Lys Ile Ile Glu Glu Tyr Lys Phe Glu Ser Asn Glu Pro Glu Asn
        115                 120                 125
gtt ccg gtt ttg gat gag acg agt gat ttg ttc cgc agg ttt agg cag    432
Val Pro Val Leu Asp Glu Thr Ser Asp Leu Phe Arg Arg Phe Arg Gln
    130                 135                 140
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aaa aaa cga gat gcc ttg gtc gat agc aag aag att gag atc tat gag    480
Lys Lys Arg Asp Ala Leu Val Asp Ser Lys Lys Ile Glu Ile Tyr Glu
145                 150                 155                 160
gag ttt gac act gtt gca tat tgg aaa cag aag gcg ttg agt ctt gag    528
Glu Phe Asp Thr Val Ala Tyr Trp Lys Gln Lys Ala Leu Ser Leu Glu
                165                 170                 175
aaa atg ctt gag gcg agt act gag aga gaa agg cga ttg atg gag aag    576
Lys Met Leu Glu Ala Ser Thr Glu Arg Glu Arg Arg Leu Met Glu Lys
            180                 185                 190
ctg agt gag agt ttg aaa act atg gag agt cag tca gca ccg gtc caa    624
Leu Ser Glu Ser Leu Lys Thr Met Glu Ser Gln Ser Ala Pro Val Gln
        195                 200                 205
gag ctt act cag aat ctt aag aga gct gaa ggt ttc ttg cat ttc ata    672
Glu Leu Thr Gln Asn Leu Lys Arg Ala Glu Gly Phe Leu His Phe Ile
    210                 215                 220
ctt cag aat gca cct att gtt atg ggc cat cag gtaaagtaaa aggtgattct  725
Leu Gln Asn Ala Pro Ile Val Met Gly His Gln
225                 230                 235
tgatcttgtt ttcgatcttt tcgacttttc tgattctttg ttacttatga gtttcag     782
gat aaa gat tta cgc tac ttg ttc atc tac aac aag tat cct agt tta    830
Asp Lys Asp Leu Arg Tyr Leu Phe Ile Tyr Asn Lys Tyr Pro Ser Leu
                240                 245                 250
cgg gaa cag gttagaagaa aacttttttct tctgttggat ttattgaatc            879
Arg Glu Gln
attctcttga ggaaatgtgt ttaaatcaaa atctgtttct tactatattt cag gac     935
                                                        Asp
                                                        255
att ttg gga aaa aca gac gtg gag ata ttc cat gga ggt gga gtt aaa    983
Ile Leu Gly Lys Thr Asp Val Glu Ile Phe His Gly Gly Gly Val Lys
                260                 265                 270
gaa tct gaa gat ttc aag aga gaa gtt ctt gag aaa gga aaa gct tca   1031
Glu Ser Glu Asp Phe Lys Arg Glu Val Leu Glu Lys Gly Lys Ala Ser
            275                 280                 285
aag aga gaa atc aca ttt act aca gat tta ttt gga tca aag acg ttt   1079
Lys Arg Glu Ile Thr Phe Thr Thr Asp Leu Phe Gly Ser Lys Thr Phe
        290                 295                 300
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ttg ata tat gtt gag cct gtt tac aac aaa gct ggc gag aaa atc ggt   1127
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    305                 310                 315
ata aac tac atg gga atg gaa gta act gat cag gttagttagc taaagatttt 1180
Ile Asn Tyr Met Gly Met Glu Val Thr Asp Gln
320                 325                 330
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ag gta gtg aaa agg gag aaa atg gcg aaa ctt aga gaa gat aac gct    1287
   Val Val Lys Arg Glu Lys Met Ala Lys Leu Arg Glu Asp Asn Ala
                  335                 340                 345
gtg aga aag gcg atg gaa tca gaa ctg aac aag act att cac att aca   1335
Val Arg Lys Ala Met Glu Ser Glu Leu Asn Lys Thr Ile His Ile Thr
                350                 355                 360
g gtttgttcaa gttaagcact gaaagtttta gaaagattaa tgagaaaact         1386
agacttaggt gttgtgtttt ttcttttgca g ag gag aca atg aga gca aag cag 1440
                                  Glu Glu Thr Met Arg Ala Lys Gln
                                                  365
atg cta gcg acg atg tct cat gag ata agg tca cca ttg tca gga gta   1488
Met Leu Ala Thr Met Ser His Glu Ile Arg Ser Pro Leu Ser Gly Val
370                 375                 380                 385
gtg gga atg gct gag ata ctt tca act aca aaa ctg gat aaa gag caa   1536
Val Gly Met Ala Glu Ile Leu Ser Thr Thr Lys Leu Asp Lys Glu Gln
                390                 395                 400
aga cag ttg ttg aat gtc atg atc tct tct ggt gat ttg gtg ctt cag   1584
Arg Gln Leu Leu Asn Val Met Ile Ser Ser Gly Asp Leu Val Leu Gln
            405                 410                 415
cta atc aac gac att ctt gat ctc tcc aag gtt gaa tca g gtacaatata  1634
Leu Ile Asn Asp Ile Leu Asp Leu Ser Lys Val Glu Ser
        420                 425                 430
ctgttttcaa agtttttgat cttgtggtgt ggtcattgtt caaatcctcg attacatatg 1694
ttatttttg gtatttgtgt gttcttttta g gt gtg atg aga tta gaa gct aca 1748
                                  Gly Val Met Arg Leu Glu Ala Thr
                                                  435
aag ttt cga cca aga gaa gta gtg aag cat gtg cta cag aca gct gca   1796
Lys Phe Arg Pro Arg Glu Val Val Lys His Val Leu Gln Thr Ala Ala
    440                 445                 450
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gca tcg ctg aag aaa tct ttg aca tta gaa gga aac att gca gat gat   1844
Ala Ser Leu Lys Lys Ser Leu Thr Leu Glu Gly Asn Ile Ala Asp Asp
455                 460                 465                 470
gtt cct att gag gttactacac atttcagaaa gagttaaatg tggcaaaagt       1896
Val Pro Ile Glu
ctttgtgatc ttaacttttt ttcctttaaa tgtttag gta gtt gga gat gtt      1948
                                        Val Val Gly Asp Val
                                        475
cta agg att agg cag atc ctc acc aat ttg ata ag gttctttacc        1993
Leu Arg Ile Arg Gln Ile Leu Thr Asn Leu Ile Ser
480                 485                 490
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cag c aat gct atc aag ttt aca cat gaa gga aat gta gga atc aaa     2099
      Asn Ala Ile Lys Phe Thr His Glu Gly Asn Val Gly Ile Lys
                495                 500                 505
ctc caa gtg ata tca gaa cca tcc ttt gtg cgg gat aac gca ttg aac   2147
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                510                 515                 520
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Ala Asp Thr Glu Glu His Glu Gln Asn Gly Leu Thr Glu Thr Ser Val
            525                 530                 535
tgg att tgc tgt gac gta tgg gac act gga att gga atc cca           2237
Trp Ile Cys Cys Asp Val Trp Asp Thr Gly Ile Gly Ile Pro
        540                 545                 550
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ctaacctata tattaacctg gttcatgttt tggtgttctt gtgcag aa aac         2339
                                                  Glu Asn
gct ctt cca tgt ttg ttc aag aag tac atg caa gca agc gct gat cat   2387
Ala Leu Pro Cys Leu Phe Lys Lys Tyr Met Gln Ala Ser Ala Asp His
    555                 560                 565
gcc cga aaa tac ggt ggg act ggt ctc gga ctt gct att tgt aaa cag   2435
Ala Arg Lys Tyr Gly Gly Thr Gly Leu Gly Leu Ala Ile Cys Lys Gln
570                 575                 580                 585
ctg gtaagctatt attaggattt tacaacacta cagaagaaac taatgaagct        2488
Leu
cgttatccta atctttctct gtttgtttac ag gtt gag tta atg gga ggc caa   2541
                                    Val Glu Leu Met Gly Gly Gln
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ctc act gtg aca agc cgg gtg aac gaa ggt tca acg ttc aca ttt ata   2589
Leu Thr Val Thr Ser Arg Val Asn Glu Gly Ser Thr Phe Thr Phe Ile
    595                 600                 605
tta ccc tac aaa gtt gga aga tca gat gat tat tca gat gat caa gat   2637
Leu Pro Tyr Lys Val Gly Arg Ser Asp Asp Tyr Ser Asp Asp Gln Asp
610                 615                 620                 625
gag ttc tct gat atg gcg gat caa caa tct gaa cca gac gat aca gct   2685
Glu Phe Ser Asp Met Ala Asp Gln Gln Ser Glu Pro Asp Asp Thr Ala
                630                 635                 640
gaa gga tat ttc cag ttt aaa ccg ctc tta gga tcg ata tat tcg aat   2733
Glu Gly Tyr Phe Gln Phe Lys Pro Leu Leu Gly Ser Ile Tyr Ser Asn
            645                 650                 655
ggc gga ccg ggg atc agc aat gac ttc tta cct cat aaa gtc atg ctt   2781
Gly Gly Pro Gly Ile Ser Asn Asp Phe Leu Pro His Lys Val Met Leu
        660                 665                 670
act agt cct att aag ctc atc aat ggt ttt gtc gct gat ccc tct aac   2829
Thr Ser Pro Ile Lys Leu Ile Asn Gly Phe Val Ala Asp Pro Ser Asn
    675                 680                 685
aac act gga cag agc gag atg cta cag ctt gaa aac ggt ggt tac atg   2877
Asn Thr Gly Gln Ser Glu Met Leu Gln Leu Glu Asn Gly Gly Tyr Met
690                 695                 700                 705
gat gaa tct aaa ctc gaa acc agt tct ggt cat tgc cct gaa tca gct   2925
Asp Glu Ser Lys Leu Glu Thr Ser Ser Gly His Cys Pro Glu Ser Ala
                710                 715                 720
cac caa tat gag aat gga aat ggt cga tgt ttc tct aag gaa tct gaa   2973
His Gln Tyr Glu Asn Gly Asn Gly Arg Cys Phe Ser Lys Glu Ser Glu
            725                 730                 735
tct tgt agc agt tca caa gct agc tca gaa ggt gga acc tta gaa atg   3021
Ser Cys Ser Ser Ser Gln Ala Ser Ser Glu Gly Gly Thr Leu Glu Met
        740                 745                 750
gag tca gag ctc aca gtt tca tct cat agg gaa gag gaa aaa gcc gag   3069
Glu Ser Glu Leu Thr Val Ser Ser His Arg Glu Glu Glu Lys Ala Glu
    755                 760                 765
ata gaa gta aaa gaa aca tca aag cca aat att ttg ctt gtg gaa gat   3117
Ile Glu Val Lys Glu Thr Ser Lys Pro Asn Ile Leu Leu Val Glu Asp
770                 775                 780                 785
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aat aag atc aac atc atg gtt gca aag tcg atg atg aag cag tta ggc   3165
Asn Lys Ile Asn Ile Met Val Ala Lys Ser Met Met Lys Gln Leu Gly
                790                 795                 800
cat acc atg gat att gct aat aat gga gtt gaa gcc ata acc gcg att   3213
His Thr Met Asp Ile Ala Asn Asn Gly Val Glu Ala Ile Thr Ala Ile
            805                 810                 815
aat agc tct agc tac gat ctg gta ctc atg gtatgtaaat tttcttagct     3263
Asn Ser Ser Ser Tyr Asp Leu Val Leu Met
        820                 825
ctaaggactt gtccttttca aattcactta tatttgaaaa aggcttataa ttcatattgg 3323
gttcacag gat gtg tgc atg ccg gtg ctc gat ggt tta aaa gct aca      3370
         Asp Val Cys Met Pro Val Leu Asp Gly Leu Lys Ala Thr
                830                 835                 840
aga ctg atc cgt tcg tat gaa gaa act ggg aac tgg aat gct gca ata   3418
Arg Leu Ile Arg Ser Tyr Glu Glu Thr Gly Asn Trp Asn Ala Ala Ile
                845                 850                 855
gaa gcc gga gta gat ata tcg aca tcg gag aat gaa caa gtt tgt atg   3466
Glu Ala Gly Val Asp Ile Ser Thr Ser Glu Asn Glu Gln Val Cys Met
            860                 865                 870
cgt ccc aca aac cgg ctg cct ata atc gcg gtcagtactt ctttttcgaa     3516
Arg Pro Thr Asn Arg Leu Pro Ile Ile Ala
        875                 880
tactaaacac agagatctaa tgcataactt gagaaaactg atagtcagaa tgcgttgtgg 3576
aatgtgcag atg acg gca aat act tta gca gag agt tca gaa gaa tgt      3624
          Met Thr Ala Asn Thr Leu Ala Glu Ser Ser Glu Glu Cys
                885                 890                 895
tat gca aat ggt atg gac tcg ttt att tcg aaa cct gta acg ttg caa   3672
Tyr Ala Asn Gly Met Asp Ser Phe Ile Ser Lys Pro Val Thr Leu Gln
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aaa ctg aga gag tgt ttg caa cag tat ttg cac tga                   3708
Lys Leu Arg Glu Cys Leu Gln Gln Tyr Leu His
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Gln Phe Asn Val Glu Lys Pro Ala Gly Asp Leu Asp Thr Leu Lys Glu
35 40 45
Val Thr Ile Glu Thr Arg Thr Ile Ala Asp Met Thr Arg Leu Pro Asn
50 55 60
Leu Leu Asn Ser Thr His Gln Gly Ser Ser Gln Leu Thr Asn Leu Val
65 70 75 80
Lys Gln Trp Glu Tyr Met Gln Asp Asn Ala Val Arg Leu Leu Lys Glu
85 90 95
Glu Leu Lys Asn Leu Asp Arg Gln Arg Glu Glu Ala Glu Ala Lys Glu
100 105 110
Leu Lys Ile Ile Glu Glu Tyr Lys Phe Glu Ser Asn Glu Pro Glu Asn
115 120 125
Val Pro Val Leu Asp Glu Thr Ser Asp Leu Phe Arg Arg Phe Arg Gln
130 135 140
Lys Lys Arg Asp Ala Leu Val Asp Ser Lys Lys Ile Glu Ile Tyr Glu
145 150 155 160
Glu Phe Asp Thr Val Ala Tyr Trp Lys Gln Lys Ala Leu Ser Leu Glu
165 170 175
Lys Met Leu Glu Ala Ser Thr Glu Arg Glu Arg Arg Leu Met Glu Lys
180 185 190
Leu Ser Glu Ser Leu Lys Thr Met Glu Ser Gln Ser Ala Pro Val Gln
195 200 205
Glu Leu Thr Gln Asn Leu Lys Arg Ala Glu Gly Phe Leu His Phe Ile
210 215 220
Leu Gln Asn Ala Pro Ile Val Met Gly His Gln Asp Lys Asp Leu Arg
225 230 235 240
Tyr Leu Phe Ile Tyr Asn Lys Tyr Pro Ser Leu Arg Glu Gln Asp Ile
245 250 255
Leu Gly Lys Thr Asp Val Glu Ile Phe His Gly Gly Gly Val Lys Glu
260 265 270
Ser Glu Asp Phe Lys Arg Glu Val Leu Glu Lys Gly Lys Ala Ser Lys
275 280 285

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Arg Glu Ile Thr Phe Thr Thr Asp Leu Phe Gly Ser Lys Thr Phe Leu
    290                 295                 300
Ile Tyr Val Glu Pro Val Tyr Asn Lys Ala Gly Glu Lys Ile Gly Ile
305                 310                 315                 320
Asn Tyr Met Gly Met Glu Val Thr Asp Gln Val Val Lys Arg Glu Lys
                325                 330                 335
Met Ala Lys Leu Arg Glu Asp Asn Ala Val Arg Lys Ala Met Glu Ser
            340                 345                 350
Glu Leu Asn Lys Thr Ile His Ile Thr Glu Glu Thr Met Arg Ala Lys
        355                 360                 365
Gln Met Leu Ala Thr Met Ser His Glu Ile Arg Ser Pro Leu Ser Gly
    370                 375                 380
Val Val Gly Met Ala Glu Ile Leu Ser Thr Thr Lys Leu Asp Lys Glu
385                 390                 395                 400
Gln Arg Gln Leu Leu Asn Val Met Ile Ser Ser Gly Asp Leu Val Leu
                405                 410                 415
Gln Leu Ile Asn Asp Ile Leu Asp Leu Ser Lys Val Glu Ser Gly Val
            420                 425                 430
Met Arg Leu Glu Ala Thr Lys Phe Arg Pro Arg Glu Val Val Lys His
        435                 440                 445
Val Leu Gln Thr Ala Ala Ala Ser Leu Lys Lys Ser Leu Thr Leu Glu
    450                 455                 460
Gly Asn Ile Ala Asp Asp Val Pro Ile Glu Val Val Gly Asp Val Leu
465                 470                 475                 480
Arg Ile Arg Gln Ile Leu Thr Asn Leu Ile Ser Asn Ala Ile Lys Phe
                485                 490                 495
Thr His Glu Gly Asn Val Gly Ile Lys Leu Gln Val Ile Ser Glu Pro
            500                 505                 510
Ser Phe Val Arg Asp Asn Ala Leu Asn Ala Asp Thr Glu Glu His Glu
        515                 520                 525
Gln Asn Gly Leu Thr Glu Thr Ser Val Trp Ile Cys Cys Asp Val Trp
    530                 535                 540
Asp Thr Gly Ile Gly Ile Pro Glu Asn Ala Leu Pro Cys Leu Phe Lys
545                 550                 555                 560
Lys Tyr Met Gln Ala Ser Ala Asp His Ala Arg Lys Tyr Gly Gly Thr
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Gly Leu Gly Leu Ala Ile Cys Lys Gln Leu Val Glu Leu Met Gly Gly
            580                 585                 590
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```
Gln Leu Thr Val Thr Ser Arg Val Asn Glu Gly Ser Thr Phe Thr Phe
        595                 600                 605
Ile Leu Pro Tyr Lys Val Gly Arg Ser Asp Asp Tyr Ser Asp Asp Gln
    610                 615                 620
Asp Glu Phe Ser Asp Met Ala Asp Gln Gln Ser Glu Pro Asp Asp Thr
625                 630                 635                 640
Ala Glu Gly Tyr Phe Gln Phe Lys Pro Leu Leu Gly Ser Ile Tyr Ser
                645                 650                 655
Asn Gly Gly Pro Gly Ile Ser Asn Asp Phe Leu Pro His Lys Val Met
            660                 665                 670
Leu Thr Ser Pro Ile Lys Leu Ile Asn Gly Phe Val Ala Asp Pro Ser
        675                 680                 685
Asn Asn Thr Gly Gln Ser Glu Met Leu Gln Leu Glu Asn Gly Gly Tyr
    690                 695                 700
Met Asp Glu Ser Lys Leu Glu Thr Ser Ser Gly His Cys Pro Glu Ser
705                 710                 715                 720
Ala His Gln Tyr Glu Asn Gly Asn Gly Arg Cys Phe Ser Lys Glu Ser
                725                 730                 735
Glu Ser Cys Ser Ser Ser Gln Ala Ser Ser Glu Gly Gly Thr Leu Glu
            740                 745                 750
Met Glu Ser Glu Leu Thr Val Ser Ser His Arg Glu Glu Glu Lys Ala
        755                 760                 765
Glu Ile Glu Val Lys Glu Thr Ser Lys Pro Asn Ile Leu Leu Val Glu
    770                 775                 780
Asp Asn Lys Ile Asn Ile Met Val Ala Lys Ser Met Met Lys Gln Leu
785                 790                 795                 800
Gly His Thr Met Asp Ile Ala Asn Asn Gly Val Glu Ala Ile Thr Ala
                805                 810                 815
Ile Asn Ser Ser Ser Tyr Asp Leu Val Leu Met Asp Val Cys Met Pro
            820                 825                 830
Val Leu Asp Gly Leu Lys Ala Thr Arg Leu Ile Arg Ser Tyr Glu Glu
        835                 840                 845
Thr Gly Asn Trp Asn Ala Ala Ile Glu Ala Gly Val Asp Ile Ser Thr
    850                 855                 860
Ser Glu Asn Glu Gln Val Cys Met Arg Pro Thr Asn Arg Leu Pro Ile
865                 870                 875                 880
Ile Ala Met Thr Ala Asn Thr Leu Ala Glu Ser Ser Glu Glu Cys Tyr
                885                 890                 895
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Ala Asn Gly Met Asp Ser Phe Ile Ser Lys Pro Val Thr Leu Gln Lys
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Leu Arg Glu Cys Leu Gln Gln Tyr Leu His
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